

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 05:25:18 ; Search time 1497 Seconds  
(without alignments)  
9793.993 Million cell updates/sec

Title: US-10-808-964A-2  
Perfect score: 1773  
Sequence: 1 ggcactccgtgattgttc.....caatcgcttgggtacc 1773

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_Main:\*

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1773	100.0	1773	6	US-10-314-512-2
2	1773	100.0	1773	8	US-10-808-964-2
3	1285.2	72.5	1768	7	US-10-311-423-4
4	1278.8	72.1	1768	7	US-10-311-423-2
5	1277.2	72.0	1768	7	US-10-311-423-6
6	1274	71.9	1768	7	US-10-311-423-3
7	1274	71.9	1768	7	US-10-311-423-5
8	1252	70.6	1762	7	US-10-311-423-1
9	1218.2	68.7	1759	7	US-10-311-423-7
10	1196.8	67.5	17460	5	US-10-038-001-7
11	1195.8	67.4	5225	5	US-10-286-186-16
12	1195.8	67.4	5285	5	US-10-038-001-1
13	1195.8	67.4	5650	5	US-10-038-001-2
14	1195.8	67.4	5650	6	US-10-286-186-17
15	1059.8	59.8	1759	3	US-09-784-962-5
16	1059.8	59.8	1759	3	US-09-884-514-5
17	1059.8	59.8	1759	9	US-10-624-049-5
18	1059.8	59.8	1759	9	US-10-780-318-5
19	1058.4	59.7	1768	6	US-10-314-512-1
20	1058.4	59.7	1768	8	US-10-808-964-1
21	981.2	55.3	1768	3	US-09-784-962-3
22	981.2	55.3	1768	3	US-09-884-514-3
23	981.2	55.3	1768	8	US-10-624-049-3

C	24	981.2	55.3	1768	9	US-10-780-318-3	Sequence 3, Appli
C	25	976.4	55.1	1768	3	US-09-784-962-4	Sequence 4, Appli
C	26	976.4	55.1	1768	3	US-09-884-514-4	Sequence 4, Appli
C	27	976.4	55.1	1768	8	US-10-624-049-4	Sequence 4, Appli
C	28	976.4	55.1	1768	9	US-10-780-318-4	Sequence 4, Appli
C	29	967.2	54.6	1768	3	US-09-884-514-6	Sequence 6, Appli
C	30	967.2	54.6	1768	8	US-10-624-049-6	Sequence 6, Appli
C	31	967.2	54.6	1768	9	US-10-780-318-6	Sequence 6, Appli
C	32	954	53.8	1767	3	US-09-784-962-1	Sequence 1, Appli
C	33	954	53.8	1767	3	US-09-884-514-1	Sequence 1, Appli
C	34	954	53.8	1767	8	US-10-624-049-1	Sequence 1, Appli
C	35	954	53.8	1767	9	US-10-780-318-1	Sequence 1, Appli
C	36	952.4	53.7	1767	3	US-09-784-962-2	Sequence 2, Appli
C	37	952.4	53.7	1767	3	US-09-884-514-2	Sequence 2, Appli
C	38	952.4	53.7	1767	8	US-10-624-049-2	Sequence 2, Appli
C	39	952.4	53.7	1767	9	US-10-780-318-2	Sequence 2, Appli
C	40	921	51.9	1759	7	US-10-682-420-5	Sequence 5, Appli
C	41	921	51.9	1759	7	US-10-409-613-5	Sequence 5, Appli
C	42	921	51.9	1759	7	US-10-442-180-5	Sequence 5, Appli
C	43	921	51.9	1759	8	US-10-718-266-5	Sequence 5, Appli
C	44	921	51.9	1759	8	US-10-775-337-5	Sequence 5, Appli
C	45	921	51.9	1759	9	US-10-637-011-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-10-314-512-2  
; Sequence 2, Application US/10314512  
; Publication No. US20030170270A1  
; GENERAL INFORMATION:  
; APPLICANT: Meng, Xiang-Jin  
; APPLICANT: Fenaux, Martijn G.  
; APPLICANT: Halbur, Patrick G.  
; TITLE OF INVENTION: Chimeric Infectious DNA Clones, Chimeric Porcine Circoviruses and  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: AM100878  
; CURRENT APPLICATION NUMBER: US/10/314,512  
; CURRENT FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1773  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-10-314-512-2

Query Match	100.0%;	Score 1773;	DB 6;	Length 1773;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1773;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGTACCTCGTGGATTGTTCTCAGCAGTCTTCCAAAATTGCAAAATGCAAGTAGTAATCCTCCGA	60	
DB	1	GGTACCTCGTGGATTGTTCTCAGCAGTCTTCCAAAATTGCAAAATGCAAGTAGTAATCCTCCGA	60	
QY	61	TAGAGAGCTTCTACAGCTGGGACAGCTGGAGGTAGTACATCTCTGGGGGGCTGATTG	120	
DB	61	TAGAGAGCTTCTACAGCTGGGACAGCTGGAGGTAGTACATCTCTGGGGGGCTGATTG	120	
QY	121	CTGGTAATCAAAATCTCGGGGCCAAAAGCAAGTACATCCCTTTTGTCTCTACAGTC	180	
DB	121	CTGGTAATCAAAATCTCGGGGCCAAAAGCAAGTACATCCCTTTTGTCTCTACAGTC	180	
QY	181	AATGGATACCGGTCAACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAATCA	240	
DB	181	AATGGATACCGGTCAACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAATCA	240	
QY	241	TCCAAACACAACTTCTTCTCCATGATATCCATCCCAACCATTTTCTTACAGGCTTC	300	
DB	241	TCCAAACACAACTTCTTCTCCATGATATCCATCCCAACCATTTTCTTACAGGCTTC	300	
QY	301	CAGTAGGTGTCTCCTAGGCTCAGCAAAATTAACGGGGCCCACTGGCTCTTCCCAACACCGGCG	360	

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	1059.8	59.8	1759	3	US-09-347-594-5	Sequence 5, Appli
C 2	1059.8	59.8	1759	3	US-09-082-558-5	Sequence 5, Appli
C 3	1059.8	59.8	1759	3	US-09-161-092-5	Sequence 5, Appli
C 4	1059.8	59.8	1759	3	US-09-583-350-5	Sequence 5, Appli
C 5	1059.8	59.8	1759	3	US-09-884-514-5	Sequence 5, Appli
C 6	1059.8	59.8	1759	3	US-09-784-962-5	Sequence 5, Appli
C 7	1053.2	59.4	3609	3	US-09-583-545-13	Sequence 13, Appli
C 8	981.2	55.3	1768	3	US-09-347-594-3	Sequence 3, Appli
C 9	981.2	55.3	1768	3	US-09-082-558-3	Sequence 3, Appli
C 10	981.2	55.3	1768	3	US-09-161-092-3	Sequence 3, Appli
C 11	981.2	55.3	1768	3	US-09-583-350-3	Sequence 3, Appli
C 12	981.2	55.3	1768	3	US-09-884-514-3	Sequence 3, Appli
C 13	981.2	55.3	1768	3	US-09-784-962-3	Sequence 3, Appli
C 14	976.4	55.1	1768	3	US-09-347-594-4	Sequence 4, Appli
C 15	976.4	55.1	1768	3	US-09-082-558-4	Sequence 4, Appli
C 16	976.4	55.1	1768	3	US-09-161-092-4	Sequence 4, Appli
C 17	976.4	55.1	1768	3	US-09-583-350-4	Sequence 4, Appli
C 18	976.4	55.1	1768	3	US-09-884-514-4	Sequence 4, Appli
C 19	976.4	55.1	1768	3	US-09-784-962-4	Sequence 4, Appli
C 20	967.2	54.6	1768	3	US-09-082-558-6	Sequence 6, Appli
C 21	967.2	54.6	1768	3	US-09-161-092-6	Sequence 6, Appli
C 22	967.2	54.6	1768	3	US-09-583-350-6	Sequence 6, Appli
C 23	967.2	54.6	1768	3	US-09-884-514-6	Sequence 6, Appli
C 24	954	53.8	1767	3	US-09-347-594-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 05:14:52 ; Search time 7316 Seconds  
(without alignments)  
11338.641 Million cell updates/sec

Title: US-10-808-964A-2  
Perfect score: 1773  
Sequence: 1 ggtacctcggtgattgttc.....caaatcgcccttgggtacc 1773

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_gss1.\*  
10: gb\_gss2.\*  
11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	56.6	3.2	1101	10	CNS00LT2
C 2	50.2	2.8	939	10	CNS00CNG
C 3	48.6	2.7	870	2	BG445569 GA_Ha002
C 4	48.2	2.7	573	6	CD659610 EtESTef53
C 5	47.6	2.7	1141	10	AG365778 Mus_muscu
C 6	47.4	2.7	922	10	CNS0073W
C 7	47.2	2.7	912	10	AG886740 Oryza sat
C 8	46.8	2.6	451	7	CO856405 LM_SL5_00
C 9	46.8	2.6	553	7	CO824976 LM_GB5_00
C 10	46.6	2.6	571	6	CA741621 wia1c.pk0
C 11	46.6	2.6	857	3	BP162319
C 12	46.6	2.6	909	10	CNS00JTL
C 13	46.4	2.6	560	6	CA222795 SCHZF403
C 14	46	2.6	401	1	AW25252
C 15	45.6	2.6	179	7	CF963096
C 16	45.6	2.6	388	7	CF962795
C 17	45.6	2.6	389	7	CF962731
C 18	45.6	2.6	474	7	CF959714
C 19	45.4	2.6	439	8	DN145761
C 20	45.2	2.5	330	8	DR179060
C 21	45.2	2.5	415	8	DR012815
C 22	45.2	2.5	455	8	DN458173

C 23	45.2	2.5	460	7	CV144191
C 24	45.2	2.5	486	8	DR089500
C 25	45.2	2.5	522	8	DN459245
C 26	45.2	2.5	540	8	DN447345
C 27	45.2	2.5	621	7	CV137364
C 28	45.2	2.5	626	8	DN460355
C 29	45.2	2.5	649	7	CV138441
C 30	45.2	2.5	657	8	DN458986
C 31	45.2	2.5	670	7	CV138430
C 32	45.2	2.5	703	8	DN447213
C 33	45.2	2.5	708	8	DN462364
C 34	45.2	2.5	713	8	DN460425
C 35	45.2	2.5	724	8	DN449051
C 36	45.2	2.5	727	7	CV137577
C 37	45.2	2.5	729	7	CV146884
C 38	45.2	2.5	739	8	DN463011
C 39	45.2	2.5	744	7	CO413802
C 40	45.2	2.5	745	8	DN451000
C 41	45.2	2.5	757	7	CO409276
C 42	45.2	2.5	766	8	DN451374
C 43	45.2	2.5	767	7	CO410601
C 44	45.2	2.5	768	7	CV138839
C 45	45.2	2.5	769	7	CO413933

## ALIGNMENTS

RESULT 1  
CNS00LT2/c

LOCUS  
DEFINITION

ACCESSION  
KEYWORDS

VERSION  
SOURCE

ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL

COMMENT

FEATURES  
source

ORIGIN

CNS00LT2 1101 bp DNA linear GSS 14-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC:  
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

AL078714 GI:5102004  
GSS.

Drosophila melanogaster (fruit fly)  
Drosophila melanogaster

Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)  
Genoscope.

Direct Submission  
Submitted (11-JUN-1999) Genoscope - Centre National de Sequençage :

BP 131 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Ooeogawa and  
Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
PI and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers  
1. .1101

/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"

/clone="BACR48P19"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 01:18:23 ; Search time 1095 Seconds

(without alignment)  
10791.324 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggtacctcctggtgttc.....caaatggccttcgggtacc 1773

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000a:\*

4: Geneseqn2001a:\*

5: Geneseqn2001b:\*

6: Geneseqn2002a:\*

7: Geneseqn2002b:\*

8: Geneseqn2003a:\*

9: Geneseqn2003b:\*

10: Geneseqn2003c:\*

11: Geneseqn2003d:\*

12: Geneseqn2004a:\*

13: Geneseqn2004b:\*

14: Geneseqn2005a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1773	100.0	1773	9 AAL57177	AAL57177 Porcine C
2	1296.4	73.1	1767	13 ADW76756	Adw76756 Pig circ
3	1285.2	72.5	1768	6 ABX08205	ABX08205 PMWS-Porc
4	1278.8	72.1	1768	6 ABX08203	ABX08203 PMWS-Porc
5	1277.2	72.0	1768	6 ABX08207	ABX08207 CT-Porc
6	1274	71.9	1768	6 ABX08206	ABX08206 CT-Porc
7	1274	71.9	1768	6 ABX08204	ABX08204 PMWS-Porc
8	1270.8	71.7	1774	6 ABX08219	ABX08219 PMWS-Porc
9	1252	70.6	1762	6 ABX08202	ABX08202 PMWS-Porc
10	1218.2	68.7	1759	6 ABX08220	ABX08220 CT-Porc
11	1210.2	68.3	1759	6 ABX08220	ABX08220 CT-Porc
12	1196.8	67.5	1768	8 ABX08204	ABX08204 PMWS-Porc
13	1196.8	67.5	1768	8 ABX08204	ABX08204 PMWS-Porc
14	1195.8	67.4	5285	8 AAX83755	AAX83755 Porcine c
15	1195.8	67.4	5285	8 AAX83755	AAX83755 Porcine c
16	1195.8	67.4	5650	8 AAX83755	AAX83755 Porcine c
17	1195.8	67.4	5650	8 AAX83755	AAX83755 Porcine c
18	1059.8	59.8	1759	4 AAF75837	AAF75837 Porcine c
19	1058.4	59.7	1768	9 AAL57176	AAL57176 Porcine c

20	1055.6	59.5	1759	2 AAX35013	AAX35013 Nucleotid
21	1053.2	59.4	3609	4 AAF28320	AAF28320 PJ107 do
22	981.2	55.3	1768	2 AAX35380	AAX35380 Nucleotid
23	981.2	55.3	1768	2 AAX35212	AAX35212 Nucleotid
24	981.2	55.3	1768	3 AAZ56871	AAZ56871 DNA seque
25	981.2	55.3	1768	3 AAZ56871	AAZ56871 PCV DNA f
26	976.4	55.1	1768	2 AAX35381	AAX35381 Nucleotid
27	976.4	55.1	1768	2 AAX35213	AAX35213 Nucleotid
28	976.4	55.1	1768	3 AAZ56872	AAZ56872 DNA seque
29	976.4	55.1	1768	4 AAF75838	AAF75838 PCV DNA f
30	976.4	55.1	1768	2 AAX35382	AAX35382 Nucleotid
31	967.2	54.6	1768	2 AAX35012	AAX35012 Genomic D
32	967.2	54.6	1768	2 AAX35214	AAX35214 Nucleotid
33	954	53.8	1767	2 AAX35378	AAX35378 Nucleotid
34	954	53.8	1767	2 AAX35210	AAX35210 Nucleotid
35	954	53.8	1767	2 AAZ56869	AAZ56869 DNA seque
36	954	53.8	1767	4 AAF75835	AAF75835 PCV DNA f
37	952.4	53.7	1767	2 AAX35379	AAX35379 Nucleotid
38	952.4	53.7	1767	2 AAX35211	AAX35211 Nucleotid
39	952.4	53.7	1767	3 AAZ56870	AAZ56870 DNA seque
40	952.4	53.7	1767	4 AAF75836	AAF75836 PCV DNA f
41	921	51.9	1759	2 AAX85593	AAX85593 Nucleotid
42	916.2	51.7	1759	2 AAX87992	AAX87992 Porcine c
43	742.2	41.9	1361	2 AAX83757	AAX83757 Porcine c
44	740.6	41.8	1786	2 AAX83755	AAX83755 Porcine c
45	738.4	41.6	1768	8 ABV72527	ABV72527 Nucleotid

## ALIGNMENTS

### RESULT 1

AAL57177 standard; DNA; 1773 BP.

XX AAL57177;

DT 27-OCT-2003 (revised)

DT 09-OCT-2003 (first entry)

XX Porcine circovirus type 1-2 chimeric DNA.

XX Porcine circovirus type 2; PCV1-2; PMWS; weaning piglet; dyspnoea;  
KW progressive weight loss; postweaning multisystemic wasting syndrome; ds;  
KW tachypnea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene;  
KW viral infection; chimeric.

XX Porcine circovirus type 1.

XX Porcine circovirus type 2.

XX Chimeric.

XX Key Location/Qualifiers

FT CDS 959..1659

FT /tag= a

FT /product= "Porcine circovirus type 2 ORF2 capsid protein"

XX WO2003049703-A2.

XX 19-JUN-2003.

XX 11-DEC-2002; 2002WO-US039646.

XX 12-DEC-2001; 2001US-0340775P.

XX 08-NOV-2002; 2002US-0424840P.

XX 09-DEC-2002; 2002US-00314512.

XX (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.

XX (IOWA ) UNIV IOWA STATE RES FOUND INC.

XX PA Meng X, Fenaux M, Halbur PG;

XX PI WPI; 2003-513959/48.

XX DR P-PSDB; AAO23063.

